From Page No.___

Sent 8 samples back to microchemistry to read from other end. — MΦ #'s 902, 904, 908, 911, 912, 913, 917, 918

DNA SEQUENCING REQUEST
Microchemistry Department

Requested by Heather Pearson .... Date

Notebook Reference(required): 95-1065 p. 13 Project: 16

Vector: PRC CMV Host: XL #of Clones 8
(Please indicate size)
913
Names of Sample(s): MΦ 902 904 ~~908~~ 908, 911, 912, 917, 959
(Please provide OD260 and insert size)

Sequencing Primer(s): OC03
(Note: sequencing primers should be at 5ug/ml)

Check one
☐ Long run (~14 hrs/~550bp)
☒ Short run (~7hrs/~300bp) Data can be provided the same day samples are run

Check one
☒ DS-DNA template (we need 1ug/rxn. or primer)
☐ SS-DNA template (we need 500ug/rxn. or primer)
☐ PCR fragment (amt. we need depends on size and purity)
☐ Phage lysate

All templates will be sequenced with Taq-Dye Terminator Chemistry.

Other Instructions:

MΦ 902 MC 17701 HS. cDNA Clone 1   100%(65/65) T90395
MΦ 904 MC 17702 HS. cDNA clone 5'end SE   96%(246/255) T32201
MΦ 908 MC 17704 HS. cDNA clone 112   98%(207/210) T85702
911 MC 17705 hum. glycoprotein MRNA   63%(157/248) N80922
912 MC 17706 Rat nov. sprague dawley col. 62%(106/170) U0 8836
913 MC 17703 Bovine microsatellite   68%(42/61) L37 252
917 MC 17707 Bact. Sequence
~~918~~
959 MC 17708 HS. cDNA clone 78116 3 78% (12/128) T61622

ABI PRISM

Model 373A
Version 2.0.1A

mc17705
DCO3 primer
MO911
Lane 32

Signal G:175 A:123 T:51 C:51
DyeTerminator(AnyPrimer)
197 MATRIX FILE
Points 343 to 8144   Base 1: 343

Spacing: 11.63 Adaptive
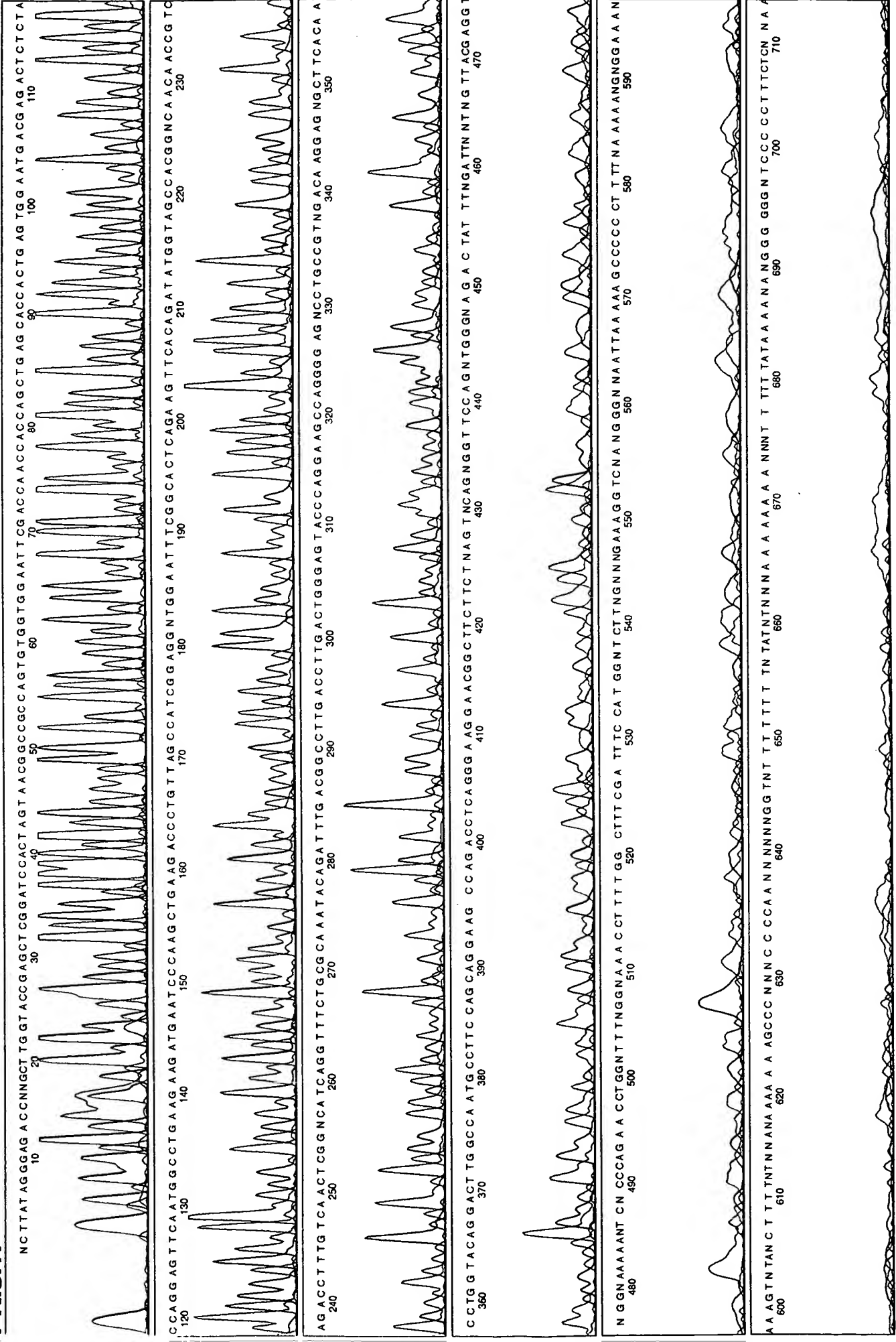
Subject: Re: 17705

From: "NCBI BLAST E-Mail Server" <blast@ncbi.nlm.nih.gov>

To: Heather Pearson

```
→gb|M80927|HUMHA3G     Human glycoprotein mRNA, complete cds.      427   6.2e-26   1
 gb|U19900|SSU19900    Sus scrofa 38kDa heparin-binding gly...     358   4.6e-20   1
 gb|U02270|MSU02270    Manduca sexta chitinase mRNA, comple...     308   8.2e-16   1
 gb|M57601|BACCHIA3    B.circulans chitinase A1 (chiA) gene...     223   1.2e-08   1
 gb|L14614|TRRENDOCHI  Trichoderma harzianum endochitinase ...     173   0.00020   1
emb|X79381|THECH42     T.harzianum (IMI 206040) ech-42 gene.       173   0.00020   1
emb|X64104|AACHI1A     A.album chi1 gene for chitinase             130   0.56      1
 gb|U13646|CELZK783    Caenorhabditis elegans cosmid ZK783. .      129   0.65      1
dbj|D12647|STMCHIC     S.lividans gene for chitinase C, com...     124   0.93      1
 gb|M82804|STMCHTA     Streptomyces plicatus chitinase 63 (...     124   0.93      1
 gb|T92100|T92100      ye01h11.r1 Homo sapiens cDNA clone 1...     123   0.94      1
emb|X15208|SMCHIB      Serratia marcescens chiB gene for ch...     119   0.9991    1
emb|Z36295|SHCHITB     S.marcescens (BJL200) chiB gene for ...     119   0.9991    1
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>gb|M80927|HUMHA3G Human glycoprotein mRNA, complete cds.
            Length = 1741
  Plus Strand HSPs:
 Score = 427 (118.0 bits), Expect = 6.2e-26, P = 6.2e-26
 Identities = 157/248 (63%), Positives = 157/248 (63%), Strand = Plus / Plus
Query:     2 ACCAACCACCAGCTGAGCACCACTGAGTGGAATGACGAGACTCTCTACCAGGAGTTCAAT 61
             | |||| | ||  |    |||| ||||||||||||| | ||| |||||        | |||
Sbjct:   255 AGCAACGATCACATCGACACCTGGGAGTGGAATGATGTGACGCTCTACGGCATGCTCAAC 314

Query:    62 GGCCTGAAGAAGATGAATCCCAAGCTGAAGACCCTGTTAGCCATCGGAGGNTGGAATTTC 121
             ||  ||||| | |||  ||||| |||||||||| || ||  |  |||||||| ||||| ||
Sbjct:   315 ACACTCAAGAACAGGAACCCCAACCTGAAGACTCTCTTGTCTGTCGGAGGATGGAACTTT 374


>gb|U19900|SSU19900 Sus scrofa 38kDa heparin-binding glycoprotein mRNA,
            complete cds. >emb|Z47803|SSGP38KD S.scrofa 38kDa heparin-binding
            glycoprotein.
            Length = 1733
  Plus Strand HSPs:
 Score = 358 (98.9 bits), Expect = 4.6e-20, P = 4.6e-20
 Identities = 148/245 (60%), Positives = 148/245 (60%), Strand = Plus / Plus
Query:     2 ACCAACCACCAGCTGAGCACCACTGAGTGGAATGACGAGACTCTCTACCAGGAGTTCAAT 61
             | |||| | ||  |    ||||  ||||||||||||| | ||| |||||  |     | ||
Sbjct:   250 AGCAACAATGAGATTGACACCTTGGAGTGGAATGATGTGACGCTCTATGACACACTGAAC 309

Query:    62 GGCCTGAAGAAGATGAATCCCAAGCTGAAGACCCTGTTAGCCATCGGAGGNTGGAATTTC 121
             ||  |||||  | ||  ||||||  |||||||||| ||  |  |  |||||| |||| ||
Sbjct:   310 ACACTCAAGAACAGGAACCCCAACCTGAAGACCCTCCTGTCTGTTGGAGGATGGAACTTT 369


>gb|U02270|MSU02270 Manduca sexta chitinase mRNA, complete cds.
            Length = 2452
  Plus Strand HSPs:
 Score = 308 (85.1 bits), Expect = 8.2e-16, P = 8.2e-16
 Identities = 110/172 (63%), Positives = 110/172 (63%), Strand = Plus / Plus
Query:    76 GAATCCCAAGCTGAAGACCCTGTTAGCCATCGGAGGNTGGAATTTCGGCACTCAGAAGTT 135
             | ||||||| |||||  ||| ||  | ||||  | || || || ||| |  |||| | ||
Sbjct:   309 GCATCCCAGCGTCAAGTTCATGGTAGCGGTGGGCGGCTGGGCTGAAGGCAGTTCGAAGTA 368
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